

# SEQUENCE LISTING

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<110> Olsen et al.

<120> Stanniocalcin Polynucleotides, Polypeptides, and Methods Based
      Thereon

<130> PF108P2

<140> US 09/840,989
<141> 2001-04-25

<150> PCT/US00/29432
<151> 2000-10-26

<150> US 60/161,740
<151> 1999-10-27

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<170> PatentIn version 3.1

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tca gca gtg ctt ctg gtg ctg gtg atc agt gct tct gca acc cat gag      104
Ser Ala Val Leu Leu Val Leu Val Ile Ser Ala Ser Ala Thr His Glu
5              10              15              20

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gcg gag cag aat gac tct gtg agc ccc agg aaa tcc cga gtg gcg gcc Ala Glu Gln Asn Asp Ser Val Ser Pro Arg Lys Ser Arg Val Ala Ala 25 30 35	152
caa aac tca gct gaa gtg gtt cgt tgc ctc aac agt gct cta cag gtc Gln Asn Ser Ala Glu Val Val Arg Cys Leu Asn Ser Ala Leu Gln Val 40 45 50	200
ggc tgc ggg gct ttt gca tgc ctg gaa aac tcc acc tgt gac aca gat Gly Cys Gly Ala Phe Ala Cys Leu Glu Asn Ser Thr Cys Asp Thr Asp 55 60 65	248
ggg atg tat gac atc tgt aaa tcc ttc ttg tac agc gct gct aaa ttt Gly Met Tyr Asp Ile Cys Lys Ser Phe Leu Tyr Ser Ala Ala Lys Phe 70 75 80	296
gac act cag gga aaa gca ttc gtc aaa gag agc tta aaa tgc atc gcc Asp Thr Gln Gly Lys Ala Phe Val Lys Glu Ser Leu Lys Cys Ile Ala 85 90 95 100	344
aac ggg gtc acc tcc aag gtc ttc ctc gcc att cgg agg tgc tcc act Asn Gly Val Thr Ser Lys Val Phe Leu Ala Ile Arg Arg Cys Ser Thr 105 110 115	392
ttc caa agg atg att gct gag gtg cag gaa gag tgc tac agc aag ctg Phe Gln Arg Met Ile Ala Glu Val Gln Glu Glu Cys Tyr Ser Lys Leu 120 125 130	440
aat gtg tgc agc atc gcc aag cgg aac cct gaa gcc atc act gag gtc Asn Val Cys Ser Ile Ala Lys Arg Asn Pro Glu Ala Ile Thr Glu Val 135 140 145	488
gtc cag ctg ccc aat cac ttc tcc aac aga tac tat aac aga ctt gtc Val Gln Leu Pro Asn His Phe Ser Asn Arg Tyr Tyr Asn Arg Leu Val 150 155 160	536
cga agc ctg ctg gaa tgt gat gaa gac aca gtc agc aca atc aga gac Arg Ser Leu Leu Glu Cys Asp Glu Asp Thr Val Ser Thr Ile Arg Asp 165 170 175 180	584
agc ctg atg gag aaa att ggg cct aac atg gcc agc ctc ttc cac atc Ser Leu Met Glu Lys Ile Gly Pro Asn Met Ala Ser Leu Phe His Ile 185 190 195	632
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agg aga cgc acc aat gag ccg cag aag ctg aaa gtc ctc ctc agg aac Arg Arg Arg Thr Asn Glu Pro Gln Lys Leu Lys Val Leu Leu Arg Asn 215 220 225	728
ctc cga ggt gag gag gac tct ccc tcc cac atc aaa cgc aca tcc cat Leu Arg Gly Glu Glu Asp Ser Pro Ser His Ile Lys Arg Thr Ser His 230 235 240	776
gag agt gca taa ccagggagag gttattcaca acctcaccaa actagtatca Glu Ser Ala 245	828

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Tyr	Ser	Lys	Leu	Asn	Val	Cys	Ser	Ile	Ala	Lys	Arg	Asn	Pro	Glu	Ala
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Ile Thr Glu Val Val Gln Leu Pro Asn His Phe Ser Asn Arg Tyr Tyr  
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Asn Arg Leu Val Arg Ser Leu Leu Glu Cys Asp Glu Asp Thr Val Ser  
 165 170 175

Thr Ile Arg Asp Ser Leu Met Glu Lys Ile Gly Pro Asn Met Ala Ser  
 180 185 190

Leu Phe His Ile Leu Gln Thr Asp His Cys Ala Gln Thr His Pro Arg  
 195 200 205

Ala Asp Phe Asn Arg Arg Arg Thr Asn Glu Pro Gln Lys Leu Lys Val  
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Leu Leu Arg Asn Leu Arg Gly Glu Glu Asp Ser Pro Ser His Ile Lys  
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Arg Thr Ser His Glu Ser Ala  
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Arg Phe Ser Ser Asn Ser Pro Ser Asp Val Ala Arg Cys Leu Asn Gly  
 35 40 45

Ala Leu Ala Val Gly Cys Gly Thr Phe Ala Cys Leu Glu Asn Ser Thr  
 50 55 60

Cys Asp Thr Asp Gly Met His Asp Ile Cys Gln Leu Phe Phe His Thr  
 65 70 75 80

Ala Ala Thr Phe Asn Thr Gln Gly Lys Thr Phe Val Lys Glu Ser Leu  
 85 90 95

Arg Cys Ile Ala Asn Gly Val Thr Ser Lys Val Phe Gln Thr Ile Arg  
100 105 110

Arg Cys Gly Val Phe Gln Arg Met Ile Ser Glu Val Gln Glu Glu Cys  
115 120 125

Tyr Ser Arg Leu Asp Ile Cys Gly Val Ala Arg Ser Asn Pro Glu Ala  
130 135 140

Ile Gly Glu Val Val Gln Val Pro Ala His Phe Pro Asn Arg Tyr Tyr  
145 150 155 160

Ser Thr Leu Leu Gln Ser Leu Leu Ala Cys Asp Glu Glu Thr Val Ala  
165 170 175

Val Val Arg Ala Gly Leu Val Ala Arg Leu Gly Pro Asp Met Glu Thr  
180 185 190

Leu Phe Gln Leu Leu Gln Asn Lys His Cys Pro Gln Gly Ser Asn Gln  
195 200 205

Gly Pro Asn Ser Ala Pro Ala Gly Trp Arg Trp Pro Met Gly Ser Pro  
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Pro Ser Phe Lys Ile Gln Pro Ser Met Arg Gly Arg Asp Pro Thr His  
225 230 235 240

Leu Phe Ala Arg Lys Arg Ser Val Glu Ala Leu Glu Arg Val Met Glu  
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ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca acccccatcg 360  
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catccccggga' tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480  
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ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600  
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660  
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<210> 6  
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<223> Contains a BamHI restriction enzyme site followed by 6 nucleotide  
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n in eukaryotic cells.

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<210> 8  
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<212> DNA  
<213> Artificial Sequence

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8.

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<210> 9  
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 s resembling the efficient signal for translation.

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<220>  
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